ACYLTRANSFERASE
Inventors: David W. LEUNG et al.
Docket No.: 077319-0381



Figure 1

Met Asp Leu Trp Pro Gly Ala Trp GGGGACAGCCCCCCCACTTCCTACCGCTATGGGCCCAACCTCCCACTCC CACCTCCCTCCATCGGCCGGGCTAGGACACCCCCAAATCCCGTCGCCC CCTTGGCACCGACCCCGACAGAGACAGAGACACAGCCATCCGCCACCA CCGCTGCCGCAGCCTGGCGAGGGGGCCCAGCCCCCAGGCCCCCTAC CCA GGG GCA TGG 1 GGAAGTCAGCAGGCGTTGGGGGGGGGGGGGGAATAGCGGCGGCAGC TTG TGG CCCTCTGAGGTGGCCAGA ATG GAT 301 101 201 51 51 151

20 니 Phe CTG CTC TTC Leu Leu Leu CTG CTG Leu Phe TTCLeu CTC Leu CTGLeu CTGLeu CTG 10 Leu CTGMet ATG 343

Lys AAG Ala CCC AGT GCC Ser Pro Ser TGC AGC CysPhe TTC Trp CCC ACC CTG TGG Leu Thr Pro Leu CIG

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Figure 1 (continued)

 \mathcal{O} 口 ATC Trp GGC TGG G1yAsn TAC AAT TYrTTCPhe 40 Ala gcc Met AAG ATG LysPhe Phe TAC 418

Val GTG Cys Ala CCC CTC GCC ATC CCT GTG TGT Pro Val Ile Val Leu Ala GTG 50 Ala TTC CTG GCT Phe Leu 455

 \mathcal{O} 口 Arg CGTLeu TTGIle ATC AAG LysATG Met Asn GAG AAC Glu GTC Val Asn AAC Arg CGC G1yGGA 9 Arg CGA 493

Arg CGA ATC Gly 999 Tyr TAC CTG TAC Leu TYrLysCAC ATC AAA Ile His Leu CICLeu CIGMet ATG en 530

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TTC Figure 1 (continued) CAC CAC GCTCGA GGG GTG

GAG

GTG

568

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 ${
m LCG}$

CCC

 \mathcal{Q} Ser Pro Pro Phe His His 90 Ala G1yArg Val Glu Val

Leu Ser TCC AAC CAC CAG AGC TCT Ser Gln Ser Asn His GTC Val Val GTT100 Val GTT TYr \mathtt{TAT} Pro CCC ln 605

 \mathcal{O} E Gly Arg CGC 120 CCA GGC Pro CTGLeu GTA Val Glu GAG Met ATG GGG ATG Gly Met Leu Leu CTT110 CTGAsp GAT 643

GCT GGC Trp Ala GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG Leu Glu Leu Lys Arg Ala Ile Pro Val γS GI 680

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Figure 1 (continued)

Д Ile GGA GTC ATC Val G1yGCA Ala Trp Leu CTG140 TGG Cys $_{
m LGC}$ CCC Leu Ala CTG ${ t G1y}$ GGG Ala CCC Ser TCT718

Val CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC Ser I1eLys Arg Thr Gly Asp Ala 150 Arg Asp GAC Ile ATC he 755

> Ç Gln Asp 170 GAC CAG Thr ACC Gln Thr Leu Leu CTCCIGTCT GAG GTC GCC CAG ACC Ala Glu Val Ser 160 Met ATG 793

CCT GAG GGA ACG AGA AAC CAC Glu Gly Thr Arg Asn His Pro m LLLPhe GTG Val TGG Trp GTC Val AGG 830

1

180

Figure 1 (continued)

ATG CTG CCC TTC AAA CGT GGC GCC TTC C 二 Phe Gly Ala Pro Phe Lys Arg 190 Leu Met GGC TCC Ser G1yAAT Asn 868

CCC ATA Ile Pro GIC Val ATTIle CCC Pro AT CTT GCA GTG CAG GCC CAG GTT Gln Ala Gln Val 200 Leu Ala Val 1.S 905

G C 220 AAG LysTGC AAG LysCysTAC Tyr $T^{T}C$ Phe GAC Asp Gln CAA TAC Tyr TCC Ser Ser $_{
m LCC}$ ATG Met 210 GTCVal 943

GTG Val TCG GGA CAA TGT CAG GTG CGG Gln Val Arg CysGly Gln Ser ACC Thr TTCPhe CGC Arg CGTArg AG

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ACG GAA GGG CTG ACA CCA Glu Gly Leu Thr Figure 1 (continued) Thr CCC ProGTG Val CCA Pro

CCC

CTG

1018

Pro

Leu

G

GAT

K

Asp

Pro

240

GAC AGA GTC CGG CAC TCC ATG Met Ser His Arg Val Arg Asp CCA GCT CTG GCT Leu Ala 250 Ala Pro GTC Val AC 1055

Ü Ö TIC CGG GAA AIC ICC ACT GAT GGC CGG 270 Gly Arg Asp Thr Ser Ile Glu Phe Arg GTT Val ACT Thr 260 CTCLeu 1093

GT GGT GGT TAT CTG AAG AAG CCT GGG GGC GGT GGG TGA ACCCTGGCTCTGAGCTCTCCTCCCATCTGTCCCCATCTTCCTCCC CACACCTACCCACCCAGTGGGCCCTGAAGCAGGGCCAAACCCTCTTCCTT GTCTCCCCTCTCCCCACTTATTCTCCTCTTTGGAATCTTCAACTTCTGAA ly Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly 280 1130 1266 1168

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Figure 1 (continued)

ACTCTTGCCTCGGTGCAGTTTCCACTCTTGACCCCCACCTCCTACTGTCT TGTCTGTGGGACAGTTGCCTCCCCCTCATCTCCAGTGACTCAGCCTACAC **AAGGGAGGGAACATTCCATCCCCAGTGGAGTCTCTTCCTATGTGGTCTT** CTCTACCCCTCTACCCCCACATTGGCCCAGTGGACTCATCCATTCTTTGGA ACAAATCCCCCCCCCTCCAAAGTCCATGGATTCAATGGACTCATTT TGTGAGGAGGACTTCTCGCCCTCTGGCTGGAAGCTGATACCTGAAGCACT TGTAGCCTCCTGTCAGTGGGGGCTGGACCCTTCTAATTCAGAGGTCTCAT GCCTGCCCTTGCCCAGATGCCCAGGGTCGTGCACTCTCTGGGATACCAGT TCAGTCTCCACATTTCTGGTTTTCTGTCCCCATAGTACAGTTCTTCAGTG GACATGACCCCACCCAGCCCCTGCAGCCCTGCTGACCATCTCACCAGAC ACAAGGGGAAGAAGCAGACATCAGGTGCTGCACTCACTTCTGCCCCCTGG GGAGTTGGGGAAAGGAACGAACCCTGGCTGGAGGGGATAGGAGGGCTTTT 1316 1466 995 1366 1416 1516 616 1666 1766 1816 1716 1966 1916 1866

Figure 1 (continued)

5 AATTTATTTCTTTTTCTGTTGAGGCTTCCCCCTCTCTGAGCCAGTTTTCA	5 TTTCTTCCTGGTGGCATTAGCCACTCCCTGCCTCTCACTCCAGACCTGTT	CCCACACACTGGGGAGGTAGGCTGGGAGCAAAAGGAGGGGGGGG	5 TTTTGCGTGGTTGTTTTTTTATTATTATCTGGATAACAGCAAAAAACTG
2016	2066	2116	2166

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2216 AAAATAAAGAGAGAGAAAAAAAA

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50 <u>F</u> <u>F</u> KMA G E	100 -YGIRVEVRG MLGLDVK -FGLKVECRK WAGVKVQLHA	150 -VPI-AKRELVTAKKSL TVTV-GKKSL STLAVMKKSS	200 LTQDVRVWV- KKNKRALWV- KKRRISIWM- KDFPRPFWLA	250 LAVQAQVPIV LAQQGKIPIV AAIAAGVPII SAVSIMRDFY
40 LWFCSPSAKY C ILVCVFGSIY LIVNAIQAVL	PLMLLHIKYL ARCFYHVMKL GHMFGRLAPL WLQLVWVVDW	140 VLPGRC IFPPGCT- IVQ-PP ILAQRSGCLG	190 SVMSEVAQTL DTLNKGLENV GTIAEVVNHF KTLKWGLQRL	240 MLPFKRGAFH MLPFKKGAFH -LPFKTGAFH VLIPRTKGFV
30 LL-LLFLLPT AL-AG RL-IITVIYS PLGLLFLLSG	80 GRNVENMKIL GKQHLAQWIT PRNPKHVATF	130 SLDLLGMME STLDIFMLGR NNYDMVTASN SDIDWL-IGW	180 IDRKRTGDAI LDRSKRQEAI IDRNNRTKAH LERS-WAKDE	230 T T ASQGLPAPRN
20 <u>LLL</u> LLF YLRSV <u>L-VVL</u> <u>LYIF</u> <u>PL</u> V <u>LVVL</u>	70 VLAIPVCAVR VIASILCTLI CLFS EL	120 -PYVVVSNHQ KPYIMIANHQ -NAIYIANHQ EHALIISNHR	170 WLAGVIE WFMALSGTYE WLTGNLL WFAEYLE	220 GS SEL RGLAKLLAAQEYA
10 <u>M</u> DLWPGAWM- <u>M</u> SV-IGRFLY <u>M</u>	60 FYNGWILFLA FYGG FYRINRFLA	110 AHHF-PPSQ- VVGE-ENLAK PTDA-ESYG- DEETYRSMGK	160 LWAGSAGLAC KYVPFLG LWIPFFGQLY KFLPVIGWSM	210 -FPEGTRNHN -FPEGTRSYT -FPEGTRSRG LFVEGTRFTP
ਜਿਜਜ	51 51 51 51	101 101 101 101	151 151 151 151	201 201 201 201
Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT

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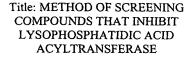
Figure 2 (continued)

Least LPAAT 251 PIVMSSYQDF YCKKERRFTS GQCQVRVLPP VPTEGLTPDD VPN VPAST LLPAAT 251 PVVVSSNTSTL VSFRYGVENR GCMIVRILKP GCNITORILK GGONGKDQ VRN Maize LPAAT 251 PVCVSTTSNK I—NIARLHN GLVIVEWILPP IDVSQYGKDQ VRN Maize LPAAT 251 PVCVSTTSNK I—NIARLHN GLVIVEWILPP IDVSQYGKDQ VRN Maize LPAAT 251 PAIYDTT—V IVPKDSPQPT MIRILKGQSS VIHVRMKRHA MSS 310 330 340 350 400 340 350 400 370 380 390 400 400 420 LPAAT 351 -AIEX—A AL——Q HDKKVNKKIK NEPVPSVSIS NDF E.coli LPAAT 351 -AIEX—A AL———Q HDKKVNKKIK NEPVPSVSIS NDF E.coli LPAAT 351 -AIEX—A AL———Q HDKKVNKKIK NEPVPSVSIS NDF E.coli LPAAT 351 FGAIEFFKWT QLLSTWRGVA FTAAGMALVT GVMHVFINFS QAHUMAN LPAAT 361 SCOli LPAAT 361		0	VPALADR		MSEMPKSDED	0	*	1 1 1 1 1 1 1 1 1	*	<u>Y</u> TLFWSCLLL	0	•	NDVNTHNEGS		QAERS	C	•	•	•	•
251 PIVMSSYQDF YCKKERRETS 251 PVVVSNTSTL VSPKYGVENR GCQVRVLPP 251 PVVVSNTSTL VSPKYGVENR GCMIVKILKP 251 PVCVSTTSNK I—-NLNRLHN GLVIVEMLPP 251 PAIYDTT—-V IVPKDSPQPT MLRILKGQSS 310 320 330 301 VRHSMLTV—F REISTDGRGG 301 VRDQMVDT—L KEIGYSPAIN 301 VSKWCKDIFV AKDALLDKHL ATGTFDEEIR 351AIEY—-A AL—Q HDKKVNKKIK 351AIEY—Q KKMH* 401 S—		290 30										•					•	•	•	•
251 PIVMSSYQDF 251 PVVVSNTSTL 251 PVCVSTTSNK 251 PVCVSTTSNK 251 PAIYDTTV 301 301 301 VSKWCKDIFV 351AIEYA T 351AIEYA T 351 FGAIEFFKWT 401 SV T 401 SV	(-		330					380	•					•	•		•
251 251 17 251 18 301 301 301 301 301 301 301 301 301 301		270	YCKKERRFTS VSPKYGVFNR	INLNRLHN	IVPKDSPQPT	320	VRHSMLTV-F	VRDQMVDT-L	CRSIMEOK-I	AKDALLDKHL	370	•	AL0	•	Q <u>r</u> lstwrgva	420	•	KKMH*	•	KKE*
		260	PIVMSSYODE	PVCVSTTSNK	PAIYDTTV	310	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	VSKWCKDIFV	360	•	AIEYA	•	FGAIEFFKWT	410	•	NS		SSARAARNRV
Human LPAAT E.coli LPAAT Maize LPAAT Yeast LPAAT Yeast LPAAT Maize LPAAT Human LPAAT Yeast LPAAT Keast LPAAT Yeast LPAAT Yeast LPAAT E.coli LPAAT Keast LPAAT Keast LPAAT Keast LPAAT Maize LPAAT Maize LPAAT			251	251	251		301	301	301	301		351	351	351	351		401	401	401	401
		;	Human LPAAT Yeast LPAAT	E.coli LPAAT	Maize LPAAT		Human LPAAT	Yeast LPAAT	E.coli LPAAT	Maize LPAAT		Human LPAAT	Yeast LPAAT	E.coli LPAAT	Maize LPAAT		Human LPAAT	Yeast LPAAT	E.coli LPAAT	Maize LPAAT

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60	120	180	240	300	360	420	480	540
GCCGTGTCTG	CGAGTTCTAC	CTCGCTCGTC	CTGGTTCGTG	CAGGCTGCAG	GATGGGCCTC	CTTCCTGGGG	GCGCTCTAGC	CCTCAAAGTG
30 40 50 TCGGGCGCCG GGCCGGGCCA TGGAGCTGTG	90 100 110 GTGCTGCTGA GCCGCGCGCGC	140 150 160 170 CCCTGTACTG CGCCGTGTGC TTCACGGTGT CCGCCGTGGC	230 GCATCATCGG	290 GGGACCCGCG	350 TCCTGGACAT	410 GGGAGCTGCT	470 TCAACCGGCA	530 TCAGGGAGAA
40	100	160	220	280	340	400	460	520
GGCCGGGCCA	GTGCAGCTGA	TTCACGGTGT	GAGAACATGA	TTCGAGGTGC	CACCAGAGCA	ATCGCCAAGC	GTCTTCTTCA	GAGCGCATGG
30		150	210	270	330	390	450 · 460	510
TCGGGCGCCG		CGCGCTGTGC	CCGGACGGTG	CGGGCTCCGC	CGTCTCCAAC	CTGCGTGCAG	CCTCGGGGC GTCTTCTTCA	CGACCTGGGC
20	80	140	200	250	310 320 330 340 350	380	440	490 530 540 540 520 520 530 540 ACTGCCATGA CAGTGATGG COTCAAAGTG
GGCGGCGCCG	TGCTGTTGCT	CCCTGTACTG	GCCACGGCGG	CGAAGCTTCA AGTACTTTTA	GAGGCCCGTC CCTGTGTCAT CGTCTCCAAC CACCAGAGCA TCCTGGACAT	TTCCGGAGCG	TCATCATGTA	
10	70	130	190	250	310	370	430	490
GGAGCGAGCT		GCCAAGGTCG	TGCCTGCTGT	CGAAGCTTCA	GAGGCCCGTC	ATGGAGGTCC	CCCGTGGGCC	ACTGCCATGA



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Figure 3 (continued)

600	660	720	780	840	900	960	1020	1080
Taagaagggc	CTCTTCCTTC	AGTGCAGGTG	CGTGGACACC	GGAGAACGGG	GGGCATGACC	CTCCCGGCTT	AGGAAGCCCC	CAGCTGGACC
560 570 580 590 CCGAGGGTAC TCGCAACGAC AATGGGGACC TGCTGCCTTT	650 CCGTGGTGTA	670 680 690 700 710 720 TCCTCCTTCT ACAACACCAA GAAGAAGTTC TTCACTTCAG GAACAGTCAC AGTGCAGGTG	760 770 GCGGCGGACG TCCCTGCGCT	820 830 840 CACATCTCCA AGACCCCCCA GGAGAACGGG	870 880 890 900 GCAGCCGGCC CAGTAGCCCA GACCACGGCA GGGCATGACC	910 920 930 940 950 TGGGGAGGGC AGGTGGAAGC CGATGGCTGG AGGATGGGCA GAGGGGACTC CTCCCGGCTT	1010 CCCGGGAAGC	1030 1040 1050 1060 1060 1070 1080 TTCTGTCACT GGTCTCCCT GGTGTCCCCT GCAGGGGGGCT CAGCTGGACC
580	640	700		820	880	940	1000	1060
AATGGGGACC	CCCATCGTCC	TTCACTTCAG		CACATCTCCA	CAGTAGCCCA	AGGATGGGCA	TCTCACTCAG	GGTGTCCCCT
570	630	690	750	800	870	930	990	1050
TCGCAACGAC	GGCACAGGTG	GAAGAAGTTC	CGGCCTCACT	CCATGAGGAC CACCTTCCTC	GCAGCCGGCC	CGATGGCTGG	CTCCCCCAGC	ACAGGCCCCT
	610 GCCTTCTACC TGGCAGTCCA	680 ACAACACCAA	730 740 CTGGAAGCCA TCCCCACCAG		860 GGTCTGGCGT	920 AGGTGGAAGC	980 CTCTGTCCGG	1040 GGTCTCAGAC
550	610	670	730	790	850	910	970	1030
TGGATCTATC	GCCTTCTACC	TCCTCCTTCT	CTGGAAGCCA	TGCCACCGGG	GCCACTGCGG	TGGGGAGGGC	CCAAATACCA	TTCTGTCACT

Figure 3 (continued)

1090 1100 1110 1120 1130 1140 CTCCCGGGC TCGAGGGCAG GGACTCGCGC CCACGGCACC TCTGGGNGCT GGGNTGATAA	1150 1160 1170 1180 1190 1200 AGATGAGGCT TGCGGCTGTG GGCTGAGCC ACAAGGCCCC CGATGGCCCA	1210 1220 1230 1240 1250 1260 GGAGCAGATG GGAGGACCCCAGGA GTCCCAGACT CACGCACCT GGGCCACAGG	1320 GTCAGCACTG	1380 AAAAAAAAA	1440
1130	1190	1250	1310	1370	1430
TCTGGGNGCT	ACAAGGCCCC	CACGCACCCT	AATCTGTGGG	AAAAAAAAA	
1120	1180	1240	1300	1360	1420
CCACGGCACC	GGGCTGAGCC	GTCCCAGACT	TGGCCTGAAG	TCTTGGAAAA	
1110	1170	1230	. 1290	1350	1410
GGACTCGCGC	GCCCGCTGGT	GAGGCCAGGA	CTGCTCCTGC	ATAAACACAC	
1100	1160	1220	1270 1280 1290 1300 1310 1320	1330 1340 1350 1360 1370 1380	1400
TCGAGGGCAG	TGCGGCTGTG	GGAGGACCCC	GAGCCGGGAA TCGGGGCCTG CTGCTCCTGC TGGCCTGAAG AATCTGTGGG GTCAGCACTG	TACTCCGTTG CTGTTTTTT ATAAACACAC TCTTGGAAAA AAAAAAAAA AAAAAAAAA	
1090	1150	1210	1270	1330	1390
CTCCCGGGC	AGATGAGGCT	GGAGCAGATG	GAGCCGGGAA	TACTCCGTTG	AAA

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4 Figure

CCG 50 TGG Trp Leu CTGGAG Glu Met GGAGCGAGCTGGCGCCGTCGGGCGCCGGGCCGGGCC ATG 30 20

CTG Leu 20 CAG Gln GTG Val 90 CTG Leu Leu CTG CIGLeu CTGLeu Leu TTGLeu CTG Ala Leu GCG CTG Ala gcg CCC CTGLen TGT Cys

GCG Cys TAC TyrCTGLeu GTC GCC Val Ala 120 TAC GCC AAG (Lys Ala TyrPhe GAG TTC Glu 225 525 Ala Ala Ser 100

Leu 50 CTG CTG Cys Leu $_{
m TGC}$ 180 GTC Val Leu CIC Ser TCG GTG GCC Ala 170 Val Ala ggg GTG TCC Ser 160 Val TTC Phe 150 TGC CTG Leu

TGG Trp ATC GGC Gly Ile AAC ATG AGC ATC Ser Asn Met 60 GAG Glu 210 GTG ACG CGG Arg ggc Gly Gly 200 ggc His TGC Cys190

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				뇬	Figure 4 (continued)	re 4	ŭ	onti	nuec	3)				
	240			2	250			260			270			
TTC		CGA	AGC		TTC AAG	TAC	TTT	TAC	999	CTC		$T^{T}C$	GAG	GTG
Phe	Val	Arg	Ser		Lys	$\mathrm{T} \gamma \mathrm{r}$	Phe	Phe Tyr (Gly	Leu		Phe	Glu	Val
				70										80
280		- •	290			300			χ.	310		•	320	
ອອວ	GAC	CCG	ည္သည	AGG	CTG	CAG	GAG	၁၁၅		CGT CCC	${ m TGT}$	GTC	ATC	GTC
Arg	Asp		Pro Arg	Arg	Leu	Gln	Glu	Ala	Arg Pro	Pro	Cys	Cys Val	Ile	Val
									90					
	330			3,	40		` '	350			360			
TCC	AAC	CAC	CAG	AGC	AGC ATC	CTG	GAC	GAC ATG	ATG	GGC	CIC	ATG	GAG	GTC
Ser	Asn	His	Gln	Ser	Ile	Leu	Asp	Met	Asp Met Met	G1y	ren	Met	Glu	Val
				100	-									110
370		(-)	380			390			4(400		7.	410	
CTT	SSS		GAG CGC	TGC	GTG	CAG		CCC	ATC GCC AAG CGG	CGG	GAG	CTG	CTG CTC	TTC
Leu	Pro		Glu Arg	Cys	Val	Gln		Ala	Lys	Arg	Glu	Leu Leu	Leu	Phe
									120					
	420			430	30		7	440			450			
CTG	GGG		CCC GTG		GGC CTC	ATC	ATG	ATG TAC	CTC	CTC GGG	ggc	GTC	TTC	TTC
Leu	G1y	Pro	Val	Gly Leu	Leu	Ile	Met Tyr	TYT	Leu	G1y	G1y	Val	Phe	Phe
				130								-		140
460		7	470			480			490	0		Ľ	200	
ATC	AAC		CGG CAG	၁၅၁	TCT	TCT AGC	ACT	CCC	GCC ATG ACA	ACA	GTG ATG GCC	ATG		GAC
Ile	Asn		Arg Gln	Arg	Ser	Ser	Thr	Ala	Met	Thr	Val	Met Ala		Asp

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Figure 4 (continued)

TAT Tyr 170	AAG Lys	GTC Val 200	AAG Lys	GCC Ala 230
ATC Ile	90 rrr Phe	ATC (Ile		GAA (Glu 7
TGG Trp	CCT Pro	CCC	680 ACC AAG Thr Lys	CTG (Leu (
540 GTG Val	CTG	630 GTG Val	AAC Asn	720 GTG Val
AAA Lys	30 CTG Leu	CAG	0 TAC TYr	CAG Gln
CTC	580 GAC CTG ASP Leu 180	GCA (670 TTC TAC Phe Tyr 210	GTG Val
530 AAC Asn	666 G1Y	620 CAG Gln	TCC	10 ACA Thr
GAG Glu	AAT Asn	GTC Val	TCC	GTC Val
AGG Arg	570 GAC ASP	GCA Ala	660 TTC Phe	ACA Thr
520 ATG GTC Met Val 160	AAC Asn	610 TAC CTG Tyr Leu 190	TCC Ser	700 TCA GGA Ser Gly 220
	CGC Arg	61 TAC TYF 190	TCT Ser	700 TCA GG Ser G1 220
CGC Arg	560 ACT Thr	TTC	650 TAC TYr	\mathtt{ACT}
GAG Glu	5 GGT G1Y	GCC Ala	6 GTG '	TTC Phe
510 GGC Gly	GAG Glu	600 GGC Gly	GTG Val	690 TTC Phe
CTG	550 CCC Pro	AAG Lys	640 CCC Pro	AAG Lys

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	GTG	Val		(
770	CTC	Leu		(
7	gae	Ala		(
	CT	Pro Ala Leu	810	
20	GTC	Asp Val E		9
760	GAC	Asp 240		0
	gcg	Ala	800	7
	ACT GCG	Ala	ω	(
750	ACT	\mathtt{Thr}		(
!	CTC	Leu	0	0
•	GGC	$_{ m G1y}$	790	0
740	AGC	ser Gly Leu 7		1
	ACC	Thr		0
	သည	Pro	780	{
730	ATC	Ile		•

	TCC	Ser	260
	ATC	lle	
	CAC	His	
810	CTC	Leu	
	TTC	Phe	
	ACC	Thr	
800	ACC	Thr	
w	AGG	Arg	
	ATG	Met	
790	၁၁၅	Ala	
7.5	CGG	Arg	250
	CAC	His	
	TGC	Cys	
780	ACC	Thr	
	GAC	Asp	

	CAG	Gln	
098	GTG	Val	
ω	၁၅၅	Gly	
	TCT		
850	GGG	Gly	
8	ggg	Ala	270
	ACT	Thr	
	ပ္သပ္ပ	Ala	
840	GGG	Gly	
	AAC	Asn	
	GAG	$_{\rm Glu}$	
830	CCC CAG	Gln	
~	ညည	Pro	
	ACC	Thr	,
820	AAG	Lys	

920	GETGGAAGC	
910	GGGAGGGCA	
006	CATGACCTG	
068	CCG GCC CAG TAG CCCAGACCACGGCAGGGCATGACCTGGGGAGGGCAGGTGGAAGC	
880	CCCAGA	
	TAG	***
	CAG	Gln
870	\mathcal{CC}	Pro Ala Gln ***
	ნეე	Pro

940 950 960 970 980	970 980
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	CTCAGAC	1100	AGGGCAG
0	CTCCCCCAGCTCTCACTCAGCCGGGAAGCAGGAAGCCCCCTTCTGTCACTGGTCTCAGAC	1090	ACAGGCCCCTGGTGTCCCCTGCAGGGGGCTCAGCTGGACCCTCCCCGGGCTCGAGGGCAG
1040	GCCCCTTC	1080	GGACCCTC
1030	AAGCAGGAA	1070	SGCTCAGCT
1020	AGCCCGGG.	1060	CTGCAGGG
1010	CTCTCACTC		TGGTGTCCC
1000	CTCCCCCAG	1050	ACAGGCCCC

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Figure 4 (continued)

1110	1120	1130	1140	1150	1120 1130 1140 1150 1160
	GGACTCGCG	CCCACGGCACC	FTCTGGGNGCT	GGGNTGATAA	GGACTCGCCCCACGGCACCTCTGGGNGCTGGGNTGATAAAGATGAGGCTTGCGGCTGTG
1170	1180	1190	1200	1210	1180 1190 1200 1210 1220
	GCCCGCTGG	TGGGCTGAGCC	PACAAGGCCCC	CGATGGCCCA	GCCCGCTGGTGGCCTGAGGCCCCCGATGGCCAGGAGGACCCC
1230	1240	1250	1260	1270	1240 1250 1260 1270 1280
	GAGGCCAGG	AGTCCCAGACT	CACGCACCCT	3GGCCACAGG	GAGGCCAGGAGTCCCAGGCACCCTGGGCCACAGGGAGCCGGGAATCGGGGCCTG
1290	1300	1310	1320	1330	1300 1310 1320 1330 1340
	CTGCTCCTG	CTGGCCTGAAG	AATCTGTGGG	STCAGCACTG	CTGCTCCTGCTGGCTCTGTGGGGTCAGCACTGTACTCCGTTGCTGTTTTTTT
1350	1360 ATAAACACA	1360 1370 1380 ATAAACACTCTTGGAAAAAAAAAAAAAAAAAAA	1380 AAAAAAAAA	aaaaaaaa	AAA





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Figure 5

Alignment of LPAAT Sequences.

10 20 40 50 1 <u>Mee</u> Wec <u>ir</u> arithillo 1 <u>Moe</u> Wec <u>ir</u> arithillo 1	1 MAKTRUSS-L RNRRQIKP AVAATADD DKDGVFMV 1 MDASCASSFL RCRCLESCFK ASFCMSQPKD AAGOPSRRPA DADDFFTVDD	51 QL——SRABE EYAKVAL-YC ALGFTVSAVA SLVCLLGGG RTVENM-SII 51 TLWFCS BAK YFFKMAF-YN GWILFTAVLA IPVCAV—RG RNVENM-KIL 51 TLWFCS BAK YFFKMAF-YN GWILFTAVLA IPVCAV—RG RNVENM-KIL 51 G————————————————————————————————————
Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae	L.douglassi C. nucifera	Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi

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110 120 130 140 150 101 GWEVRSFXYFYGIRFEY RDPRRIQEAR PCYIVSNHOS ILLMWGIMEY 101 RLMITHIKYLYGIRVEY RGAHFFPRQ PYVVSNHOS SILDILGMEY 101 CFY-HWKLMLGLDYKY VGFENLAK-K PYIMIANHOS TILDIFMICRI 101 GHWFGRL -FT YPLFGLKVEC RKPTDAESYG NAIYIANHON NYDMVTISM 101 GHMFGRL -FT YPLFGLKVEC RKPADAENYG NAIYIANHON NYDMVTISM 101 GHIGGLY- IMIYGIPIKI QGSEHIKKRA IFTYI SNHAS PIDAFFVMM 101 GHVFGRM FT MILGNPITI EGSEFSNIRA I-YICNHAS IVDIFILIMM	151 ILPERCVOLAK REILLFIGEVGLIMYLGGV FEINRORSST AMTVMAIL 151 ILPERCVOLAK REILMAGSAGLACWIAGV IFIDRIKRIGD ALSWISEV 151 ILPGCV PIAK KSLKV PFLGVFWALSGT YFIDRSKRIGD ALSWISEV 151 VOPPTVTVGK KSLIMIPFF TGILYWVIGN IFIDRINRITK AHSTIAEV 151 VOPPTVTVGK KSLIMIPFF TGILYWVIGN IFIDRINRIK AHSTIAEV 151 VOPPTVTVGK KSLIMIPFF TGILYWVIGN IFIDRINRIAK AHSTIAEV 151 VOPPTVTVGK KSLIMIPFF TGILYWVIGN IFIDRINRIAK AHSTIAEV 151 VOPPTVTVGK KSLIMIPFF TGILYWVIGN IFIDRINRIAK AHSTIAEV 151 VOPPTVTVGK KSLIMIPFF TGILYWVIGN ILIDRINRIAK AHSTIAEV 151 TPK;TVTVTIAK KEVIWYPILG QLYTLAH IRIDRSN PAA ALGSFTM KEA
Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera	Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi

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201 GERMRENILA WILYPEGTRN DNGDL—LPF KKGAFYL—A VQAQVPIVPV 201 AQTILIQDAR WWYFPEGTRS YISELIMLPF KRGAFHL—A VQAQVPIVPI 201 LENVKRRRR IS IWWFPEGTRS YISELIMLPF KKGAFHL—A QQGYLPIVPV 201 VNHFKKRR IS IWWFPEGTRS RGRGL—LPF KTGAF—HAA ISAGVPI IPV 201 VNHFKKRR IS IWMFPEGTRS RGRGL—LPF KTGAF—HAA ISAGVPI IPV 201 VNHFKKRR IS IWMFPEGTRS RGRGL—LPF KTGAF—HAA ISAGVPI IPV 201 VRVITHKNILS IMMFPEGTRS GJGRL—LPF KTGAF—HAA IAAGVPI IPV 201 VRVITHKNILS LIMFPEGTRS GJGRL—LPF KTGAF—HAA IAAGVPI IPV 201 VRVITHKNILS LIMFPEGTRS GJGRL—LPF KTGAF—HAA IAAGVPI IPV 201 VRVITHKNILS LIMFPEGTRS GJGRL—LPF KTGAF—HFAA IAAGVPI IPV 201 ARAWYKNILS LIMFPEGTRS GJGRL—LPF KTGAF—HFATIA LQIRLPIVPM 201 ARAWYKNILS LIMFPEGTRS KTGRL—LPF KTGAF—HFATIA LQIRLPIVPM	251 VYSS FSSF YNTKKFFTS GTVTVQVLEN IPTSGLTAND VPALVDTCHR 251 VMSS YQDF YCKK FRFTS GQQQVRVLDP VPTGLTFDD VPALADRVRH 251 VWSNTSTL VSPKYGVFTR GMIVRILKP ISTENLITKDK IGEFAEKVRD 251 CVSTTS NK INLARIHN GLVTVEMLPP IDVSGYGKDQ VRELAAHCR- 251 VCSSTH NK INLARINN GLVTVEMLPP IDVSGYTKDN VRDLAA YGHE 251 VCSSTH NK INLARINN GLVTVEMLPP VDVSEXGKDQ VRELAAHCRE 251 ILTGTHLAWF TR KGIFRVRP VPITVKYLPP INTDDWIVDK IDDXV KMIHD 251 VLTGTHLAWF TR KGIFRVRP APITVKYLBP INTDDWIVDK IDDXV KMIHD 251 VLTGTHLAWF TR KGIFRVRP APITVKYLBP INTDDWIVDK INTVEMIHF
Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera	Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera

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Figure 5 (continued)

Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera	301 301 301 301 301 301 301 301	310 AMETITIHIS SMLTVEREIS OMVDILKEIG -SIMEOKIAE TOLMEKRIAE TALMEOKIAE IYVRNLPASO K TALYVRNLPASO K	AMRTTEIHIS KTROENGATA GSGVQPAQ*- SMLIVEREIS TDGRGGDYL KKPGGGG*- OMVDILKEIG YSPAINDTTL PROAIEYAAL QHDKKVNKKI KNEPVPSVSI -SIMEQKIAE LDKEVA – ER EA AGKV*- TILMEKRIAE LDKEVA – ER EA AGKV*- IYVRNILPASQ KPLGSTNR – S-K*- TALYVDHIPE SQKPLVSKGR DASGRSNS*-	330 SSGVQPAQ*	340 QHDKKVNKKI	350 KNEPVPSVSI
		360	370	380	390	
Human L.PAAT-β	351			•	•	•
Human L.PAAT-α	351			•	•	•
Yeast LPAAT	351	SINDWITHINEG	SSVKKMH*	•	•	•
E.coli L.PAAT	351		•		•	•
H.influenzae	351		•	•	•	•
S.typhimuriu	351	; 		•	•	•
L.douglassi	351			•	•	•
C. nucifera	351			•	•	•

NBD-MAG 10. A549 11. A549:LPAAT 12. substrate 10 11 12 တ 9. BPC + PLD NBD-LysoPC 6. A549 7. A549:LPAAT ∞ 8. substrate Figure 6 9 3. A549:LPAAT + lipid A 4. A549 5. A549:LPAAT S 2. A549 + lipid A 3 Bodipy-LPA l. substrate LysoPC — PERSONAL PROPERTY. MAG / FA DAG

TLC Analysis of Acyltransferase Acitvity

Docket No.: 077319-0381

Induction of TNF in A549 LPAAT or A549 cells stimulated with mTNF and IL-1

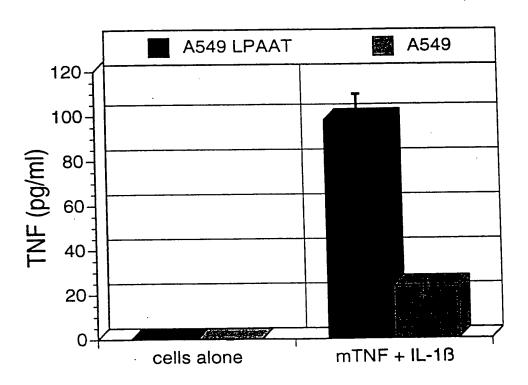


Figure 7

Docket No.: 077319-0381

Induction of IL-6 in A549 LPAAT or A549 cells stimulated with mTNF and IL-1

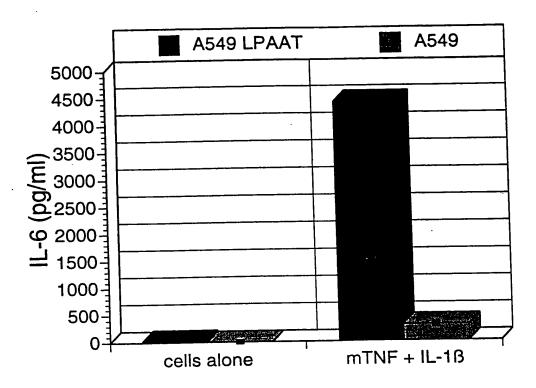


Figure 8

Inventors: David W. LEUNG et al. Docket No.: 077319-0381

Figure 9 Translated sequence of human LPAAT-γl

TCTATGAAACCAACATACATGGCGTTTGCATCACAGTTGGAGTCAGATGTGAGCCCGGAG GGCAGGTGTCTGGCTTGTCCACCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGC											60 120				
GGCĀ	GGTG	TCTG	GCTT	GTCC.	ACCC	GGAA(GCCC.	CAG	GGCA	CIG	CCC	CMCI	200 r	CACC	180
		TOCO	ጥጥርር	A C G G	ርጥርጥ	ССТС	AGCGI	\GGG	GCCG.	IGCA			LONG	CAGC	
	3 000	CCC	CTC	CTG (מכר י	ተጥር (TTG A	AAG .	ACC (CAG	TTC	GIG		CAC	225
•••	Met	Gly	Leu	Leu .	Ala	Phe 1	Leu I	jys '	Thr	GIN	Phe	Val	Leu	Hıs	
					5					10					
CTG	CTG	GTC	GGC	TTT	GTC '	TTC (GTG (GTG .	AGT	GGT	CTG	GTC	ATC	AAC	270
CIG	LOU	Wal	Glv	Phe	Val	Phe '	Val V	Val	Ser	Gly	Leu	Val	Ile	Asn	
1 -					20					25					
15	~~~	CAC	CEC	ጥርር	ACG.	CTG	GCG (CTC	TGG	CCG	GTC	AGC	AAG	CAG	315
TTC	GIC	CAG	CIG	Cvc	Thr	Leu	Ala i	Leu	Tro	Pro	Val	Ser	Lvs	Gln	
	Val	GIN	Leu	Cys	35	Dea .				40			-		
30				C.T.C	226	TGC	cec i	כתכ	GCA		TCA	CTC	TGG	AGC	360
CTC	TAC	CGC	CGC	CIC	AAC	Corn	λ×σ	7 211	Δla	ጥረድ	Ser	Len	Trp	Ser	
Leu	Tyr	Arg	Arg	Leu	ASD	Cys	Arg	Leu	AIG	55	JCI		5		
45					50		maa .	mac.	maa		NCC	GAG	TCT.	ACA	405
CAA	CTG	GTC	ATG	CTG	CTG	GAG	TGG	166	Com	Cure	WP~	Clu	Cuc	Thr	103
Gln	Leu	Val	Met	Leu	Leu	Glu	Trp	rrp	Ser	CAR	IIII	Giu	Cys	1111	
60					65					70			a. a	030	450
CTG	TTC	ACG	GAC	CAG	GCC	ACG	GTA	GAG	CGC	TTT	GGG	AAG	GAG	CAC	450
Leu	Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	hue	Gly	Lys	Glu	His	
					80					82					
	GTC	ATC	ATC	CTC	AAC	CAC	AAC	TTC	GAG	ATC	GAC	TTC	CTC	TGT	495
NI a	Val	Tle	Tle	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	
~ ~					95				1	100					
	mcc	A C C	ΔТС	ጥርጥ	GAG	CGC	TTC	GGA	GTG	CTG	GGG	AGC	TCC	AAG	540
91	166	MP~	Mor	Cve	Glu	Arg	Phe	Glv	Val	Leu	Gly	Ser	Ser	Lys	
		THE	Mec	Cys	110	**** 9		1		115	-				
105				220	CAC	CTG	CTC	TAC	GTG	CCC	CTC	ATC	GGC	TGG	585
GTC	CTC	GCT	AAG	AAG	Clu	Leu	Len	ጥረድ	Val	Pro	Leu	Tle	Glv	Tro	
Val	Leu	Ala	гЛз	гĀг	125	ьeа	Dea	- 7 -		130			4		
120					125	3 mm	CTTC	mmc	ሞርር		ccc	AAG	TGG	GAG	630
ACG	TGG	TAC	TTT	CTG	GAG	ATT	G 1 G	Dha	Cura	Luc	7~~	Tare	Trn	Glu	
Thr	Trp	Tyr	Phe	Leu	Glu	Ile	vai	Pne	Cys	145	Arg	пуз	TIP	Gia	
135					140				ama.		ccc	CTC	mcc	CAC	675
GAG	GAC	CGG	GAC	ACC	GTG	GTC	GAA	GGG	CIG	AGG	3	tou	100	Aco	3,3
Glu	Asp	Arg	Asp	Thr	Val	Val	Glu	GIY	Leu	Arg	Arg	Leu	261	Asp	
					155					TOO					720
TAC	: ccc	GAG	TAC	ATG	TGG	TTT	CTC	CTG	TAC	TGC	GAG	ال ال	ACG	CGC	720
Tvr	Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	GIU	GIY	Thr	Arg	
					170					1/3					2.55
		GAG	ACC	AAG	CAC	CGC	GTT	AGC	ATG	GAG	GTG	GCG	GCT	GCT	765
Phe	Th	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	ı Val	Ala	. Ala	Ala	
400					185					エフロ	,				
			י ככיו	GTC	CTC	AAG	TAC	CAC	CTG	CTG	CCG	CGG	ACC	AAG	810
AAC	- 63	r Tay	Dro	Val	Leu	Lvs	Tyr	His	Leu	Leu	ı Pro	Arg	Thr	Lys	
	•				700					200	,				
199			3 300	CCA	GTC	AAG	TGC	СТС	CGG	GGG	ACA	GTC	GCA	A GCT	855
GGG	2 TTC	ACC	_ ACC	. 31-	1721	Live	CVS	Leu	Aro	r Glv	/ Thr	· Val	Ala	a Ala	
		e Tu	r Tni	Ald	. va.	. Llys	CyJ		3	220)				
210	כ				215	י יאר	ጥጥር	A C A	CCA			: AAC	CCC	TCC	900
GT	C TA	r GA	r GTA	ACC	CTG	, AAC	710	AGA		. 200	n Tire	. Acr	Dro	Ser	
Va:	l Ty	r Ası	o Val	l Thr	. Leu	ı Asn	Pne	AIG	G L X	ASI	i bys	, var		Ser	
	_				237	1)				945
CT	G CT	G GG	G ATO	CTC	TAC	GGG	AAG	AAC	J.AC	GAC	ایان و	GAU	. AIC	G TGC	243
Lei	u Le	u Gl	y Ile	e Lei	ı Tyr	: Gly	Lys	Lys	з Туз	GI	T WIG	a Asp	o Mei	t Cys	
	^				745	`				231	U				000
		G AG	A TT	r cci	r cro	GAA	GAC	ATC	CCC	G CT	G GA	r GA	A AA(G GAA	990
77=] A~	g Ar	a Ph	e Pro	o Lev	ı Glu	. Asp	Ile	e Pro) Le	u Ası	o Gli	ı Lă:	s Glu	
~ ~ ~	_				760	1				20.					
23	у СС Э	т съ	ር ጥር	G CT	r CA	r aaa	CTC	TAG	CAG	G GA	G AA	G GA	CGC	G CTC	1035
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Figure 9 (continued)

Ala	Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu 280	Lys	Asp	Ala	Leu	
Gln	Glu	Ile	Tyr	Asn	CAG Gln	гÃг	GLY	1100		295	-				1080
285 AAG Lys					CCG	mcc.	» CC	CTC	CTG	AAC	TTC	CTG	TCC	TGG	1125
300 GCC Ala	ACC Thr	ATT Ile	CTC Leu	CTG Leu	305 TCT Ser	CCC Pro	CTC Leu	TTC Phe	AGT Ser	TTT	GTC Val	TTG Leu	GGC Gly	GTC Val	1170
315 TTT Phe					CCT Pro		CITIC	አጥር	CTG	ACT	TTC	TTG	GGG	TTT Phe	1215
330					335 TTT Phe	GGA Gly	cmm	ccc	AGA	CTG	АТА	GGA	GTA	ACT	1260
345		•			350 TCC: Ser	AGC Ser	ma.	CGA	220	CAA	GAG	TTT	AAG	AAA Lys	1305
360	GAA	TAA	TT!	ATGO	365 CTGT	GACI	GAAC	ACAC	:GCGC	CCC	GAC	GTGC	TATO	CAGTT	1362
Lys AAC CTC TGA	Glu CTCA GTG AAGT(AAACO ACTAZ CTTCZ	ATAT' AGCC'	ACACA PAACA PCCCA	AGAGT	TGCAC	GAAA AGCCA GGT(AAGA(AAGA(CCCA(CAATSTAA!	ragai Agaa' ETCCi rcca	AACTI PTCA(ACGC(GAAC)	ATTTT SAAGO SCGCO TCCGO	TCTT SCCT(SCGT(SCTTC	TATTAA GTCAGG GGAGG CAAGAG	1422 1482 1542 1602 1660

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Figure 10 Translated sequence of LPAAT-Y2 cDNA

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCTCAACTGCCGCCTCGCC TACTCACTCTGGAGCCTAGCACAAAACTAGAAGCAACCCAAGCACCTGTCACTGGAGAGCT AATTATGCGGCACCCATACAGGGACCCTCTGCGGCCATCATGGAGAGCCTTCATCTTGCC CGTACAGTTTTAAGCGAAAAAAGGAAGTATACAACAAAGTCCATAACTGGTC ATG CTG 238															
CGT	ACAG'	rtt <u>t</u>	<u>AA</u> GC	GAAA.	AAGG2	AAGT	ATAC	AACA	AAGT	CCA <u>T</u>	AACT	GGTC		CTG Leu	238
CTG	GAG	TGG	TGG	TCC	TGC	ACG	GAG	TGT	ACA	CTG	TTC	ACG	GAC	CAG	283
		5		Ser			10					15	_		
GCC	ACG	GTA	GAG	CGC	TTT	GGG	AAG	GAG	CAC	GCA	GTC	ATC	ATC	CTC	328
		20		Arg			25					30			
				GAG											373
		35		Glu			40					45		-	
				GTG											418
		50		Val			55					60	_	-	
				GTG											463
		65		Val			70				-	75			
				TGC											508
		80		Cys			85				_	90	_		
				CTG											553
		95		Leu			100					105	-		
				TAC Tyr											598
-		110					115					120		_	
				ATG Met											643
		125		CTG			130			_	_	135	•		400
				Leu											688
	_	140		CGG			145			_		150			722
				Arg											733
		155		GGA			160				_	165			778
				Gly											//0
		170	_	TAC		_	175					180			823
				Tyr											023
-1-	1	185	-1-	-1-			190		-1-			195			
CTG	GAA	GAC	ATC	CCG	CTG	GAT	GAA	AAG	GAA	GCA	${\tt GCT}$	CAG	TGG	CTT	868
		200		Pro			205					210	_		
				CAG											913
	-	215	-	Gln		_	220					225	-		
				TTT											958
		230		Phe			235					240	_	_	
				CTG											1003
	_	245		Leu			250					255			
				AGT											1048
Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	Ala	Ser	Gly	Ser	

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Figure 10 (continued)

		260					265					270			
CCM	CTC	260	አጥሮ	СТС	АСТ	ттс	TTG	GGG	TTT	GTG	GGA	GCA	GCT	TCC	1093
CCT	CIC	CIG	71-	7	mb~	Dhe	T 11	Gly	Phe	Val	Glv	Ala	Ala	Ser	
Pro	Leu		TTE	Leu	1111	FIIC	280	0-1			2	285			
		275							3.00	CAC	2002		* * *	ccc	1138
TTT	GGA	GTT	CGC	AGA	CTG	ATA	GGA	GTA	ACT	GAG	ATA	GAA	AAA	GGC	1130
Phe	Glv	Val	Arg	Arg	Leu	Ile	Gly	Val	Thr	GLu	Ile	GLu	Lys	GIY	
	_	290					295					300			
mcc	3.00	TAC	CCA	A A C	CAA	GAG	TTT	AAG	AAA	AAG	GAA	TAA	TTA	ATGGC	1185
TCC	AGC	IAC	GGA	AAC	01-	Clu	Dha	Lys	Lvs	Lvs	Glu	***			
Ser	Ser		GTA	Asn	GIR	GIU	210	Lys	_, _	-,-					
		305					310								1245
TGT	GACT	GAAC	ACAC	GCGG	CCT	GACG	GTGG'	ra'rc	JAG'I"	PAAC	rcaa	AACC	AACA	CACAG	1245
a cmo	CACC	מממבי	CAC	מידים ב	GAA	ACTA	$\mathbf{\Gamma}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}$	TCTT	ATTA	ACTG	GTGA(CTAA'	ratt.	AACAA	1305
2200	ኮጥር አ	CCA	ACAG	TAAAC	TAAT	rcag.	AAGG	CCTGʻ	ICAG	GTGA	AGTC'	TTCA(GCCT	CCCAC	1365
AAC	IIGA	CCA		~ x m~r	מבבים	CCC	CCC	CGTG	GGAG	GTGG	GTCC	GGCC	GGAG.	AGGCC	1425
AGC	GCAG	المالى	CAG	CAIC	ICCN			TTCC:	ADGA	CCCA	المسك	דיניי	тсст	TTCTC	1485
TCC	CGCG	GACG	CCGT	CTCT	CCAG	AACT		1100	* * *	COOK					1523
TCC'	TTAA	ACTT.	AGAT	CAAA'	TTTT.	AAAA	AAAA	AAAA	AAA						1943

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Figure 11 Translated sequence of human LPAAT- δ

TAGTTATTTATTTCTGAATAAGAGGGTCCACGCATC ATG GAC CTC GGG GAC ATG ATG CAG TCC CAG TTC CAG CTC CAC CTG GTC TCT CTG CAG GAC CTC Leu Lys Ser Gin Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe 10 ATT GCC TCA GGG CTA ATC ATC AAC ACC ATT CAG CTC TTC ACT CTC 11e Ala Ser Gly Leu Ile Ile Asn Thr Ile Gin Leu Phe Thr Leu 25 CTC CTC TGG CCC ATT AAC AAG CAC CTT CTC CGG AAG ATC AAC TGC Leu Leu Trp Pro Ile Asn Lys Gin Leu Phe Arg Lys Ile Asn Cys 40 AGA CTG TCC TAT TGC ATC TCA AGC CAG CTG GTG ATG CTG GAG ATG Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu Leu Glu 65 TGG TGG GGC ACG GAA TGC ACC ATC TTC AGC GAC CCG CGC TTP TTP Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala 85 AAG TTT CAAG TAT GGG AAG AAT GCC ATC TTC AGC GAC CCG TTP TTP Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala 85 AAG TTT GAA ATT GAC ATT TCTG TGT GGC TGT CTC AAG CAC TTP Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His 85 AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG CAA CGC Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg 100 TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCA AAA AAA GAG CTG Phe Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu 125 GCC TAT GTC CCA ATT AT ATC GGC TG ATC TGT GCC AAA AAA GAG CTG Val Phe Cys Ser Arg Lys TTP Glu Gln Asp Arg Lys Thr Val Ala 145 ACC AGT TTG CAG CAC CTC CGG GAC CAC CAC GAG CAC Val Phe Cys Ser Arg Lys TTP Glu Gln Asp Arg Lys Thr Val Ala 145 ACC AGT TTG CAG CAC CTC CGG CAG ATG ATG CTC CAG AAG AAG CAG Val Phe Cys Ser Arg Lys TTP Glu Gln Asp Arg Lys Thr Val Ala 145 ACC AGT TTG CAG CAC CTC CGG GAC TTC CCC GAG AAG AAG CAT GAG Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Try Phe Phe 160 CTG ATT CAC TTG CAC CAC ACC ACC TTC CAG CAC CAC CTC CAG ATT CAC CTG TG CAC CAC CTC CGG CAT TAC CCC CAG AAG AAG CAT GAG Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Try Phe Phe 160 CTG ATT CAC CTG TG CAC ACC ACC CTC CGC CTC CAC CTC AAG 160 ATT CAC CTG TG CAC ACC ACC CTG CTC ACC CTG CTC CTC CTC CTC CTC CTC CTC CTC C	TGAAC GAAGG	ACAC	CCCT	TCCT	CAGT	CCTG	GATC'	TTTC	TTCC	TTCT	GGAA	$\mathbf{A}\mathbf{T}\mathbf{C}\mathbf{T}$	TTGA	CTGT	GGG	61 121
Leu Lys Ser Gln Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe 10 15 20 ATT GCC TCA GGG CTA ATC ATC AAC ACC ATT CAG CTC TTC ACT CTC ILe Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln Leu Phe ATT Las 30 15 30	TAGTT	'ATTT	TTTA	CTGA	A <u>TAA</u>	GAGC	GTCC.	ACGC	ATC	ATG Met	GAC Asp	CTC Leu	GCG Ala	GGA Gly 5	CTG Leu	175
Leu Lys Ser Gln Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe 10 15 20 ATT GCC TCA GGG CTA ATC ATC AAC ACC ATT CAG CTC TTC ACT CTC ILe Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln Leu Phe ATT Las 30 15 30	CTC	A A C	ጥርጥ	CAG	ጥጥር	CTG '	TGC	CAC	CTG	GTC	TTC	TGC	TAC	GTC	TTT	220
The Ala Ser Gly Leu Ile Ile Ash Thr Ile Gln Leu Phe Thr Leu 15	Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu 15	Val	Phe	Cys	Tyr	Val 20	Phe	
The Ala Ser Gly Leu Ile Ile Ash Thr Ile Gln Leu Phe Thr Leu 15	ATT	GCC	TCA	GGG	CTA	ATC .	ATC	AAC	ACC	ATT	CAG	CTC	TTC	ACT	CTC	265
Leu Leu Trp Pro 11e Asn Lys Gln Leu Phe Arg Lys 11e Asn Cys 40 AGA CTG TCC TAT TGC ATC TCA AGC CAG CTG GTG ATG CTG CTG GAG Arg Leu Ser Tyr Cys 11e Ser Ser Gln Leu Val Met Leu Leu Glu 55 TGG TGG TGG GGC ACG GAA TGC ACC ATC TTC ACG GAC CCG CGC GCC Trp Trp Ser Gly Thr Glu Cys Thr 11e Phe Thr Asp Pro Arg Ala 70 TAC CTC AAG TAT GGG AAG AAA ACC ATC GTG GTG TC TAAC CAC Tyr Leu Lys Tyr Gly Lys Glu Asn Ala I1e Val Val Leu Asn His 85 AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG ATC GTG AAC CAC Lys Phe Glu I1e Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg 100 TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GAC AGC CTG Phe Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu 115 GCC TAT GTC CCA ATT ATC GGC TGG AGG CAC ATC AAC CAC Ala Tyr Val Pro I1e I1e Gly Trp Met Trp Tyr Phe Thr Glu Met 130 GTC TTC TGT TCG CGC AAG TG GAC CAG GAC CAC AGG GAT GAC Ala Tyr Val Pro I1e I1e Gly Trp Met Trp Tyr Phe Thr Glu Met 130 GTC TTC TGT TCG CGC AAG TG GAC CAC CAC CAC AAG AAC ACG GTT GCC Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala 155 ACC AGT TTG CAG ACC CTC CGG GAC TAC CAG ATT CAC TGT GAG AAC ACC GTT TTT CTC Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe 160 CTG ATT CAC TGT GAG GGC ACA CGG TTC AAC GAG AAG ACA GTT TTT TTC ACC AGT TTG GAG GGC ACA CGG TTC ACC GAG AAG ACA GTT TTT TTC ATC ACT GAG GTG GCC CGG GCC AAG AGC ATG CAC CTC TG GAG GAC ACA CGG TTC ACC ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG ACA TTT TTT TC ATC ACT GAG GGC ACA CGG TTC ACG GAG AAG ACA GTT TTT TTC ATC ACT GAG GTG GCC CGG GCC AAG GGC TTC ACC GTG AGG ATG CAC CTG TTG CCA CAC ACA CAC GTC ACC GTG AAG ACC ATG CAC ATG CAC ACC GTG ACC ACG GTT ACC ACC CTG TTG CCA CGA ACC ACG GTT TA ATC GAC AAG ACC GTG ACC ATG CAC CTG TTG CCA CAC ACG GTT TA ATC GAC ATC ACC CTC AAC ACC CTG TTG CCA CGA ACC ACG GTT TA ATC GAC ATC ACC CTC AAC ACC ATG CAC ATG CAC ACG GTG CCC CTC GAC AAG ACC ATC ACC CTC AAC ACC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC ATC ACC CTC AAC ACC TTG AGA AAT AAT GAA AAT CAA CAC CTC GTG GAG CTC CAC AAC ACC TTG AAA AAT CAT GAA AAT CAA CAC CTC CTG GAG	Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr 30	Ile	Gln	Leu	Phe	Thr 35	Leu	24.0
40 AGA CTG TCC TAT TGC ATC TCA AGC CAG CTG GTG ATG CTG GAG Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu Leu Glu 55 TGG TGG TGG GGC ACG GAA TGC ACC ATC TTC ACG GAC CCG CGC Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala 70 TAC CTC AAG TAT GGG AAG GAA AAT GCC ATC TTC ACG GAC CCG CGC Try Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His 90 AAG TTT GAA ATT GAC TTC TGT TGT GGC TGG AGC CTG CTC GAA CCA Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg 100 TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA AAG CTG Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met 115 GCC TAT GTC CCA ATT ATC GGC TGG ATG TTC ACG AAG AAA GAG CTG Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala 145 ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG AAA CGG TTT TTT TTC TTT Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe 160 CTG ATT CAC TGT GG GGC ACA CGG TTC Leu Ile His Cys Glu Gly Trh Arg Phe Trr Glu Lys Tyr Phe Phe 161 CTG ATT CAC TGT GG GGC ACA CGG TTC ACC AGT TGG CAC AGA CAC ACG TTC ACC AGT TGG CAC AGA CAC ACG TTC ACC AGT TGG CAC AGA CAC ACG TTC ACC AGT CAC CGG GCC AAG ACG AAG ACG CTG Try Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe 160 CTG ATT CAC TGT GGC CAC ACG TTC ACC AGT TGG CAC CGG CCC AAG ACG ACG CTT ACC CTG ATG CAC CTG CGG GAC ACG CTT ACC CTG TTG CAC CGG ACG ACG ACG TTC ACC AGT TGG CAC ACG TTC ACG GAC ACG ACG ACG ACG ACG ATG CAC CTG TGC CCG GCC AAG ACG ACG ACG ACG ATG CAC CTG TGC CCG GCC AAG ACG ACG ACG ATG CAC CTG TGC CCG GCC AAG ACG ACG ACG ATG CAC CTG TGC CCG GCC AAG ACG ACG ACG ATG CAC CTG TGC CCG ACG TTC ACC CTG TGC CCA ACG ACC ACG ACG ATG CAC CTG TGC CCG GCC AAG ACG ACG ACG ATG CAC CTG TGC CCG ACG ACG ACG ATG CAC CTG TGC CCG GCC AAG ACG ATG CAC ACG ATG ACG ACG ACG ATG CAC CTG TGC CCG ACG ACG ACG ATG CAC ACG ACG ACG ATG CAC CTG TGC CCG ACG ACG ACG CTG CCC AAG ACG ACG ACG CTG CCC CCG ACG ACG ACG CTG CCC CCG AAG ACG ACG ACG CTG CCC CCG	CTC	CTC	TGG	CCC	TTA	AAC	AAG	CAG	CTC	TTC	CGG	AAG	ATC	AAC	TGC	310
Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu Leu Glu 55 TGG TGG TGG GGC ACG GAA TGC ACC ATC TTC ACG GAC CGC GCC GCC Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala 70 TAC CTC AAG TAT GGG AAG GAA AAT GCC ATC GTG GTT CTC AAC CAC 445 Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His 90 AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG TCC GAA CGC 490 Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg 110 TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAA GAA GAG CTG 100 TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAA GAA AAA GAG CTG 110 TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAA GAA GAG CTG 125 GCC TAT GTC CAA ATT ATC GGC TGG ATG TGG TAC ACC GAA GAA CAA GAG CTG 135 GCC TAT GTC CAA ATT ATC GGC TGG ATG TGG TAC ACC GAA ATG 130 GTC TTC TGT TCG CGC AAG TCG GAA CGA CAG GAT CGC AAG AAA AAA GAG CTG 130 GTC TTC TGT TCG CGC AAG TCG GAG CAG GAT CGC AAG ACG GTT GCC 135 ACC AGT TGC CAA ATT ATC GGC TGG ACC CC GAG AAG ACG GTT GCC 625 Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala 115 ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG ACG GTT GCC 625 Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala 115 ACC AGT TGG CAG CAC CTC CGG GAC TAC CCC GAG AAG AAG CGTT TTT TTC 670 Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe 167 Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Tyr Phe Phe 170 ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG 151 ACC AGT TGC CAG GAG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG 151 ACC AGT TGC CAG AAT ATC GAG ACC AGG GCT TCC CCC CTC CAG CAC AGG ATG 151 ACC AGT TGC CAG GAG GCC CGG GCC AAG GGG CTC CCT CGC CTC AAG 151 ACC AGT TGC CAG GAG GCC CGG GCC AAG GGG CTC CCT CGC CTC AAG 151 ACC AGT TGC CAG AAA AAG GCC ACC AGG GCC TCC CCC CTC CAC ACC CTC AAG 151 ACC AGT TGC CAG AAA AAG AAG ACC AAG GGC CTC CCC CTC CAC ACC ACC ACC ACC ACC AC				40					45					50		255
TGG TGG GGC ACG GAA TGC ACC ATC TTC ACG GAC CGC GCC GCC TTTP TTP Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala 70 75 80 75 80 75 80 75 80 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 90 95 95 90 95 95 90 95 95 90 95 90 95 95 95 95 95 95 95 95 95 95 95 95 95	AGA	CTG	TCC	TAT	TGC	ATC	TCA	AGC	CAG	Lan	Unl	Mot	CIG	CTG	Clu	223
Trp Trp Ser Gly Thr Glu Cys Thr I le Phe Thr Asp Pro Arg Ala 70 75 80 75 80 75 80 75 85 80	_			55					60					65		400
TAC CTC AAG TAT GGG AAG GAA AAT GCC ATC GTG GTT CTC AAC CAC TYr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His 85 AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG TCC GAA CGC Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg 100 TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA GAG CTG Phe Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu 115 GCC TAT GTC CCA ATT ATC GGC TGG ATG TGT TCC GAA CTG Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met 130 GTC TTC TGT TCG CGC AAG TGG GAG CAG GAT CGC AAG ACG GTT GCC Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala 145 ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG ACG GTT GCC TTR Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe 160 CTG ATT CAC TGT GAG GGC CCC GGG GCC AAG AGG AAG AAG AAG	TGG	TGG	TCG	GGC	ACG	GAA	TGC	Mb~	Tla	Dha	Thr	Acn	Dro	Ara	Δla	400
Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His	_			70					75					80		445
AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG TCC GAA CGC Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg 100 TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA GAG CTG 535 Phe Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu 115 GCC TAT GTC CCA ATT ATC GGC TGG ATG TGC GAG ATG AAA GAG CTG 535 Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met 130 GTC TTC TGT TGG CGC AAG TGG GAG CAG GAT CGC AAG AAA GAG CTG 580 Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met 130 GTC TTC TGT TGG CGC AAG TGG GAG CAG GAT CGC AAG ACG GTT GCC 625 Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala 145 ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG TG TTT TTC 670 TTR Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe 160 CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT TTT TTC 670 TLE Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu 175 ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG 760 Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys 190 CAT CAC CTG TGG CAC ACG ACG ACG GTT C GCC ATC ACC GTG AGG AGG AGG AGG AGG AGG AGG AGG AGG	TAC	CTC	AAG	TAT	GGG	AAG	GAA	AAT	GCC 3.1 a	ATC	GTG	GTT	CTC	AAC	CAC	445
Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg 105 110 11				25					90					95		400
TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA GAC CTG THE Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu 115 GCC TAT GTC CCA ATT ATC GGC TGG ATG TGG TAC TTC ACC GAC ATG Ala Tyr Val Pro Ile Ile Gly Trp Met 130 GTC TTC TGT TCG CGC AAG TGG GAC CAG GAT CTC ACC GAC ATG Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala 145 ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG TATTT TTC TTC TGT TCG CGC AAG TGG GAC TAC CCC GAG AAG TATTT TTC TTC TGT TCG CAC CAC CTC CGG GAC TAC CCC GAG AAG TATTT TTC TTC TGT TGG CAC CAC CTC CGG GAC TAC CCC GAG AAG TATTT TTC TTC TGT TGG CAC CAC CTC CGG GAC TAC CCC GAG AAG TATTT TTC TTC TGT TGC CAC CAC CTC CGG GAC TAC CCC GAG AAG TATTT TTC TTC TGT TGC CAC CAC CTC CGG GAC TAC CCC GAG AAG TATTT TTC TTC TGT TGC CAC CTC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe 160 CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG T10 ETT GAG ATC CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG T10 Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys 190 CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC CTC CAAG TAC TIS His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg 200 CAT CAC CTG TTG CAC CGA ACC AGG GGC TTC GCC ACC ACC GTG AGG AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn 215 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CAC CTG GAA Phe Arg Asn Asn GAA AAT CCA ACA CTG CTG CTG CTC CAC CTG GAA ASP Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys 150 CAC ATC CCT GAA GAC GAT GAC GAC GAC GAC CTG CTG CCC CTC CAC CTG GAA ASP Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys 151 ACC ATC CCT GAA GAC GAT GAC GAC GCC CTG CCC CTG CAC AAG ASP Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys 151 ACC ATC CCT GAA GAC GAT GAC GAC CTG CCC CTG CCC CAC AAG ASP Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys 1525	AAG	TTT	GAA	TTA	GAC	TTT	CTG	TGT	GGC	TGG	AGC	CTG	TCC	GAA	CGC	490
Phe Gly Leu Leu Gly Gly Ser Lys Val				100					105					TTO		
Phe Gly Leu Leu Gly Gly Ser Lys Val	TTT	GGG	CTG	ጥጥ አ	GGG	GGC	TCC	AAG	GTC	CTG	GCC	AAG	AAA	GAG	CTG	535
SCC TAT GTC CCA ATT ATC GGC TGG ATG TGG TAC TTC ACC GAG ATG ATG ALA TYP Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met 130	Phe	Gly	Leu	Leu	Gly	Gly	Ser	Lys	Vai 120	Leu	Ala	Lys	гЛs	125	Leu	
Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met 130	GCC	ТАТ	GTC	CCA	ATT	ATC	GGC	TGG	ATG	TGG	TAC	TTC	ACC	GAG	ATG	580
STC TC TGT TCG CGC AAG TGG GAG CAG GAT CGC AAG ACG GTT GCC CGC Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala 155	Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp	Met 135	Trp	TYT	Pne	Thr	140	Met	
Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala 155	GTC	TTC	TGT	TCG	CGC	AAG	TGG	GAG	CAG	GAT	CGC	AAG	ACG	GTT	GCC	625
Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe 160 160 165 170 CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG 715 Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu 180 185 ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG 760 Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys 200 200 CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG 805 His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg 210 215 AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT 850 Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn 220 TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA 895 Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA 940 Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG CTG CTG CAC AAG 985 Asp Ile Pro Glu Asp Asp Glu Cys Ser Ala Trp Leu His Lys	Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln 150	Asp	Arg	Lys	Thr	Val 155	Ala	
Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe 160 160 165 170 CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG 715 Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu 180 185 ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG 760 Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys 200 200 CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG 805 His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg 210 215 AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT 850 Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn 220 TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA 895 Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA 940 Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG CTG CTG CAC AAG 985 Asp Ile Pro Glu Asp Asp Glu Cys Ser Ala Trp Leu His Lys	ACC	AGT	TTG	CAG	CAC	CTC	CGG	GAC	TAC	CCC	GAG	AAG	TAT	TTT	TTC	670
Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu 175 ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG 760 Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys 190 CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG 805 His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg 210 AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT 850 Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn 220 TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA 895 Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA 940 Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG CTG CTG CTG CAC AAG 985 Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	Thr	Ser	Leu	Gln	His	Leu	Arg	Asp	Tyr 165	Pro	Glu	Lys	Tyr	170	Pne	
Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu 175 ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG 760 Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys 190 CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG 805 His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg 210 AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT 850 Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn 220 TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA 895 Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA 940 Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG CTG CTG CTG CAC AAG 985 Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	CTG	ATT	CAC	TGT	GAG	GGC	ACA	CGG	TTC	ACG	GAG	AAG	AAG	CAT	GAG	715
The Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys 190 195 200 200 200 200 200 200 200 200 200 205	Leu	lle	His	Cys	Glu	Gly	Thr	Arg	Pne 180	Thr	GLu	Lys	Lys	185	GIU	
The Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys 190 195 200 200 200 200 200 200 200 200 200 205	ATC	: AGC	ATG	CAG	GTG	GCC	CGG	GCC	AAG	GGG	CTG	CCI	, CCC	CTC	AAG	760
CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg 205 AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn 220 TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	Ile	Ser	Met	Gln	Val	Ala	Arg	Ala	. Lys 195	: GTĀ	Leu	Pro	Arg	, Leu 200	ı Lys	
His His Leu Leu Pro Arg Thr Lys Gly Phe Ala He Thr Val Arg 205 AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT 850 Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn 220 TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA 895 Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA 940 Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg He Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG 985 Asp He Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	CAT	CAC	CTG	י יייים	CCA	CGA	ACC	AAC	GGC	TTC	GCC	: ATC	ACC	GTC	AGG	805
AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn 220 TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	His	: His	Lev	Leu 205	Pro	Arg	Thr	ГĀЗ	210))	Ala	ı ile	Thi	215	. Arg	
Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn 220 230 TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA 895 Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG GAG GAG GC TCG CTG CAC AAG Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	AGO	TTC	AGA	ד מ מ	CTA	GTT	TCA	. GCI	GT.	LAT A	' GAC	TGT	' AC	A CTC	TAA	850
TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA Phe Arg Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	Sea	. Lev	ı Arç	Asn	val	. Val	Ser	Ala	225	L Туг 5	Asp	Cys	Thi	230	ı Asn	
Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly 235 AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	ጥጥር	- AGA	AA?	דע בי	CAD	TAA A	CCA	ACA	A CTO	G CTC	GG?	A GTO	CT	A AAC	GGA	895
AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu 250 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	Phe	e Arg	g Asr	n Asn 235	ı Glu	ı Asn	Pro	Thi	: Let 24(ı Lev)	ı Gıy	y va.	L Le	1 ASI 249	o Giy	
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg IIe Pro Leu Glu 250 255 260 GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG 985 Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	AAC	3 AA	A TAC	י כאיז	CC	A GAT	TTC	TAT	r GT?	r ago	AG0	G ATO	CC	A CTO	G GAA	940
GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG 985 Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	Ly	s Lys	з Ту	r His	s Ala	a Asp	Leu	ı Tyı	r Va. 259	L Arg	J Ar	g Ile	e Pro	o Lei 260	a Glu	
Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	CA	ግ ልጥር	ם ככי	ר כא	GAG	GAT	GAC	GAG	G TG	C TCC	GC	C TG	G CT	G CA	C AAG	985
	As	p Ile	e Pro	o Glu	ı Ası	Asp	Asp	Gl:	T CA:	s Sei	c Al	a Tr	o Le	u Hi	s Lys	



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Figure 11 (continued)

CTC	TAC	CAG	GAG	AAG	GAT	GCC	TTT	CAG	GAG	GAG	TAC	TAC	AGG	ACG	1030
Leu	Tyr	Gln	Glu 280	Lys	Asp	Ala	Pne	Gln 285	GIU	GIU	ıyı	ığı	290	1111	
GGC	ACC	TTC	CCA	GAG	ACG	CCC	ATG	GTG	CCC	CCC	CGG	CGG	CCC	TGG	1075
Gly	Thr	Phe	Pro	Glu	Thr	Pro	Met	Val 300	Pro	Pro	Arg	Arg	Pro 305	Trp	
»CC	כיייכ	стс	295 AAC	TGG	CTG	ттт	TGG	GCC	TCG	CTG	GTG	CTC	TAC	CCT	1120
Thr	Leu	Val	Asn 310	Trp	Leu	Phe	Trp	Ala 315	Ser	Leu	Val	Leu	Tyr 320	Pro	
TTC	TTC	CAG	TTC	CTG	GTC	AGC	ATG	ATC	AGG	AGC	GGG	TCT	TCC	CTG	1165
Phe	Phe	Gln	Phe	Leu	Val	Ser	Met	Ile 330	Arg	Ser	Gly	Ser	Ser 335		
ACG	CTG	GCC	AGC	TTC	ATC	CTC	GTC	TTC	TTT	GTG	GCC	TCC	GTG	GGA	1210
Thr	Leu	Ala	Ser	Phe	Ile	Leu	Val	Phe	Phe	Val	Ala	Ser	Val 350	Gly	
GTT	CGA	TGG	ΔTG	ATT	GGT	GTG	ACG	GAA	ATT	GAC	AAG	GGC	TCT	GCC	1255
Val	Arg	Trp	Met	Ile	Gly	Val	Thr	Glu 360	Ile	Asp	Lys	Gly	Ser 365	Ala	366
TAC	GGC	AAC	TCT	GAC	AGC	AAG	CAG	AAA	CTG	AAT	GAC	TGA	CTC	AGGG	1301
Tyr	Gly	Asn	Ser 370	Asp	Ser	Lys	Gln	Lys 375	Leu	Asn	Asp	***			
ДССТ (GTC A	ССАТ	CCGA	AGGG	AACC	TTGG	GGAA	CTGG	TGGC	CTCT	GCAT	ATCC	TCCT	TAGT	1361
GGGA	CACG	CTGA	CAAA	GGCT	GGGT	GAGC	CCCI	'GCTG	GGCA	.CGGC	GGAA	GTCA	CGAC	CTCT	1421
CCAG	CCAG	CGAG	ጥርጥር	GTCT	CAAG	GCCG	GATG	GGGA	.GGAA	GATG	TTTT	GTAA	TCTT	"T"T"T"T	1481
TCCC	് മ ന്നവ	тсст	ጥጥልር	TGGG	CTTT	GGTT	TTCT	$\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}$	'GTGC	GAGT	'GTGT	'GTGA	GAAT	'GGCT	1541
GTGT	GGTG	AGTG	TGAA	CTTT	GTTC	TGTG	ATCA	TAGA	AAGG	GTAT	TTTT	GGCT	GCAG	GGGA	1601 1661
GGGC	AGGG	CTGG	GGAC	CGAA	GGGG	ACAA	GTTC	CCCI	TTCA	TCCT	"I"I'GG	TGCT	CAGI	TTTTC	1721
TGTA	ACCC	TTGG	TTGC	CAGA	GATA	AAGT	GAAA	AGTG	CTTT	AGGT	GAGA	TGAC	TAAA	TATT	1774
GCCT	CCAA	GAAA	AAAA	LTAA	AAAC	TGCT	III.C	النان	TCAP	TWWW.	MAAA	MMM	7.7		1,14

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Figure 12					
	10	20	30	40	50
_	MOLE A DEL MED	FVLHLLVGFV	FVVSGLVINF	VQ-LCTLALW	PVSKQLYRRL
LPAAT-γ1	MGDDALDKIG				
LPAAT-Y2		FLCHLVFCYV	FTASGLTINT	IO-LFTLLLW	PINKQLFRKI
LPAAT-δ	MDLAGLLKSQ	FUCHENECTA			
	60	70	80	90	100
	STATE STATE	QLVMLLEWWS	CTECTLFTDQ	ATVERFGKEH	AVIILNHNFE
LPAAT-Y1		MAT I LITATIAIS	CTECTLETDO	ATVERFGREH	WATTENUME :
LPAAT-Y2		QLVMLLEWWS	GTECTIFTDP	RAYLKYGKEN	AIVVLNHKFE
LPAAT-δ	NCRLSYCISS	Ö Γ∧₩₽₽₽₩₩2	01201211-		
	110	120	130	140	150
		ERFGVLGSSK	VLAKKELLYV	PLIGWTWYFL	EIVFCKRKWE
LPAAT-Y1			TO AKKELLYV	PI.IGWTWYFL	EIVICKRE
LPAAT-Y2	IDF LCGWIMC	ERFGVLGSSK	VLAKKELAYV	PIIGWMWYFT	EMVFCSRKWE
LPAAT- δ	IDFLCGWSES	ERFGEDGGS	,		
	160	170	180	190	
		DDI CDVDEVM	WFLLYCEGTR	FTETKHRVSM	EVAAAKGLPV
LPAAT-Y1		DOLCOVEEVM	WFLLYCEGTR	FTETKHRVSM	EVAAAKGLEV
LPAAT-Y2	EDRDIVVEGE	gnt buabasa	FFLIHCEGTR	FTEKKHEISM	QVARAKGLPR
LPAAT- δ	QDRKTVATSL	Gunkbisak:			
	210	220	230	240	
		CEMMATIKET.R	GTVAAVYDVT	LNF-RGNKNP	SLLGILYGKK
LPAAT-Y1	DDMI	CEMPANKCI.B	GTVAAVYDVT	LNF-RGNKNE	SPECTFIGER
LPAAT-Y2	PKIUPPLUI	CENTEVESIE	NVVSAVYDCT	LNF-RNNENE	LLGVLNGKK
LPAAT-δ	LKHHLLPRT	C GPALIVEDE	•		
	260	270	280		
* D. J. M. 41	VEADMCVRR!	F PLEDIPLDE	C EAAQWLHKLY	QEKDALQEI	NOKGMFPGEQ
LPAAT-γ1			z faaowi.hki.y	7 OEKDALOEI:	Y NOKGMF PGEQ
LPAAT-Y2	I EADIC VIDD	T PLEDIPEDDI	D ECSAWLHKLY	QEKDAFQEE	Y YRTGTFPETP
LPAAT-δ	YMADLIVIK	1 1222			
	31	0 32	0 330	34	0
LPAAT-Y1	FKPARRPWT	L LNFLSWATI	L LSPLFSFVLO	G VFASGSPLL	ILTFLGFV
		- TATE CLIAMT	t r.spt.EstVI.(G VFASGSPLL	T PILL PGE A
LPAAT-Y2	MUDDBBDWT	I. VNWLFWASL	V LYPFFQFLV	S MIRSGSSLT	LASFILVF
LPAAT-δ	MALLONI				
	36	io 37		-	
LPAAT-Y1	GAASFGVRF	RL IGVTEIEKG	S SYGNQEF	K KKE*	
LPAAT-γ2	CAASEGVEE	RI IGVTEIEKG	S SYGNQEF	K KKE*	
	EVACUGVRU	M IGVTEIDKG	S AYGNSDSKQ	K LND*	
LPAAT-δ	L AVOACAL				



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Figure 13

